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Processing-In-Memory (PIM) Platform for mRNA Quantification

-The study of human genetics is a rapidly expanding field, fueled in part by developments in large-scale protein and genomic sequencing technologies. Biopharmaceutical companies and modern healthcare rely heavily on sequencing technologies and the acquired data to develop new drugs and provide effective treatments to patients. However, the results obtained from genomic and nucleic acid sequencing present numerus acquisition, production, and bioinformatics challenges. The large volume of data obtained in a single sequencing experiment poses a significant logistical challenge to scientists. The resulting quality of data, which often comprises millions to hundreds of millions of small sequence reads, establishes yet another set of challenges as quantifying and verifying these results requires enormous computing power. The development of streamlined, highly automated systems and methods for genomic sequencing and data analysis is critical for transitioning the field from a technology adoption stage to a platform enabling accelerated research and results. Many obstacles are presented in developing methods, algorithms, and computing platforms for the analysis and quantification of sequencing data.

Processing-in-Memory (PIM) architecture and logic has gained traction in solving the memory-wall bottleneck and improving processing time through parallel computing, especially within bioinformatics. Recent innovation utilizing PIM for genome alignment and assembly has made great strides in the field, however an important aspect of genome analysis has been overlooked: mRNA quantification. Accurate and efficient mRNA quantification is a crucial step for molecular signature identification, disease outcome prediction, and drug development. There is a need in the art for parallel computing enabled, PIM-based architectures and algorithms to accelerate mRNA quantification.

Researchers at Arizona State University (ASU) have developed a processing-in-memory (PIM) friendly mRNA quantification algorithm. Additionally, the ASU researchers have developed an architecture that hosts and computes the data via dynamic random-access memory (DRAM) computing.

Related publication: [PIM-Quantifier: A Processing-in-Memory Platform for mRNA Quantification](#)

Potential Applications:

- Genome analysis – mRNA quantification
- Bioinformatics

Benefits and Advantages:

- PIM-based algorithm and architecture to accelerate mRNA quantification

- Compared to Von-Neumann architecture, ASU's architecture eliminates frequent data movement between data storage and computing unit to save energy and accelerate the process
- Experiments show that ASU's algorithm and architecture significantly improves mRNA quantification efficiency (i.e., throughput/power) than CPU and other recent PIM-based platforms